

CLAIMS

What is claimed is:

1. A method for biasing the amplification of one allele, said biasing being dependent on the identity of a specific nucleotide at a polymorphic site in a target nucleic acid sample, comprising:

- i) contacting a segment of DNA with two primers encompassing said polymorphic site under amplification conditions, wherein one primer contains a region at its 5' end that is not complementary to the target nucleic acid but which when incorporated into the amplification product will cause the 3' end of the strand complementary to this primer in the amplification product to form a sufficiently stable hairpin loop by hybridizing with the sequence including the polymorphic site to inhibit further amplification only if said specific nucleotide is present at said polymorphic site; and
- ii) determining whether said segment is amplified, wherein amplification of said segment is indicative that said polymorphic site contains an alternative to said specific nucleotide.

2. The method of claim 1, wherein said DNA is single stranded DNA.

3. The method of claim 1, wherein said DNA is double stranded DNA.

4. The method of claim 1, wherein the amplification of said segment is detected by detection of the presence of defined size fragments following restriction enzyme digestion of any said amplification products.

5. The method of claim 4, wherein said polymorphic site is a restriction fragment length polymorphism (RFLP), and said digestion is performed with a restriction enzyme corresponding to said RFLP, wherein the defined size fragments differ in size depending on the nucleotide present at said polymorphic site.

6. The method of claim 1, wherein said contacting and said determining is performed for each of a plurality of different polymorphic sites.

7. The method of claim 6, wherein said plurality of different

polymorphic sites provides a haplotype for a gene.

8. The method of claim 7, wherein said plurality of different polymorphic sites comprise a least one polymorphic site in a plurality of different genes.

9. The method of claim 8, wherein said plurality of different sites provides haplotypes for a plurality of different genes.

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